

Domain organization of MTSP3



FIGURE 1

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SPLICE VARIANT AND DOMAIN ORGANIZATION OF MTSP4

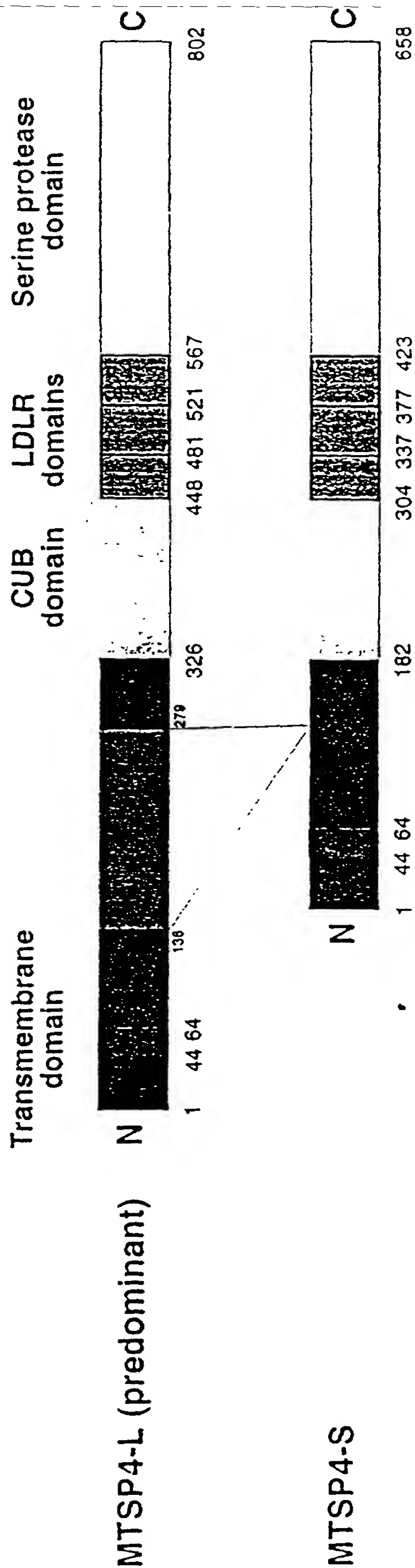


FIGURE 2

DOMAIN ORGANIZATION OF HUMAN MTSP6

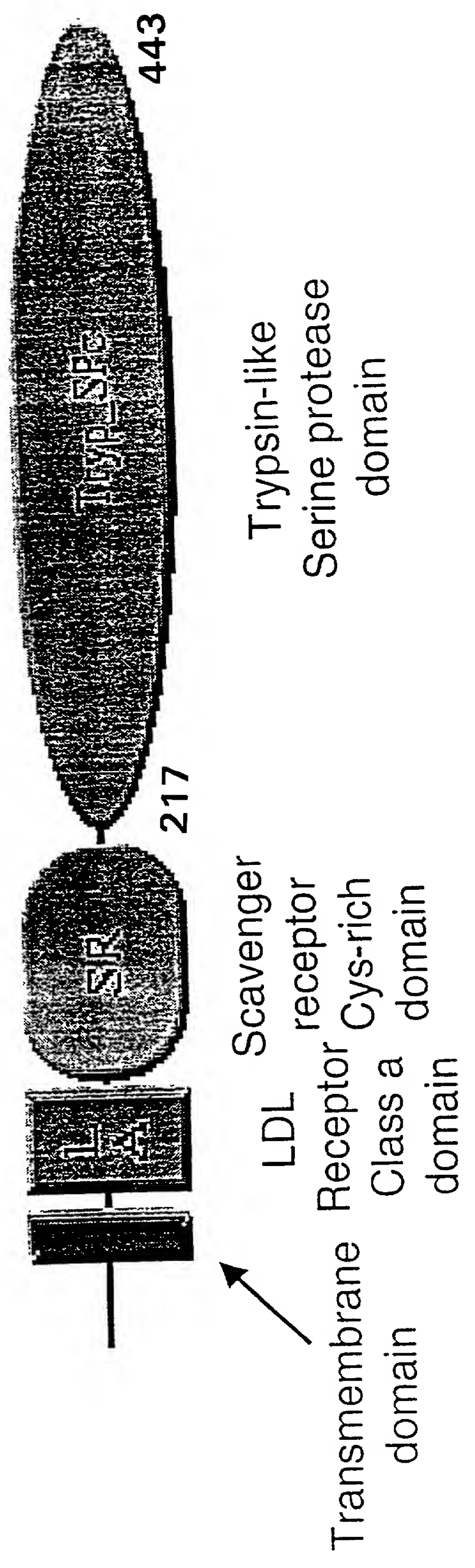


FIGURE 3

MTSP3 194 LACGKS-----LKT[▽]PRVVGGEASVDSWPWQVSIQYDKQHVC²⁰⁵CGSILD 236
 MTSP4-S 396 PQCDGRPD⁴²⁴CRDGSDEEHCECGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIA 455
 MTSP4-L 540 PQCDGRPD⁵⁶⁸CRDGSDEEHCECGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIA 599
 MTSP6 205 TACGHR-----RGYSSRIVCGNMSLLSQWPWQASLQFQGYHLCGGSVIT 248
 217 +

 MTSP3 237 PHWVLTA[▽]AHC²⁰⁵TRKIFDVTN--WKVRAGSDKLG²⁰⁵S----FPSLAVAKITIEFNPMYPKDND 290
 MTSP4-S 456 DRWVITA[▽]AHC²⁰⁵TQEDSMAS²⁰⁵TVLWTVFLGKVWQNSRWPG²⁰⁵EVSFKVSRL²⁰⁵LLHPYHEEDSHDYD 515
 MTSP4-L 600 DRWVITA[▽]AHC²⁰⁵TQEDSMAS²⁰⁵TVLWTVFLGKVWQNSRWPG²⁰⁵EVSFKVSRL²⁰⁵LLHPYHEEDSHDYD 659
 MTSP6 249 PLWILTA[▽]AHC²⁰⁵VYDLYL²⁰⁵PKS--WTIQVGLVSL²⁰⁵LD--NPAPSHLVEKIVYH²⁰⁵SKYKPKRLGND 304

 MTSP3 291 IALMKLQ[▽]FPLTFSGTVR²⁰⁵PICLPFFDEEITPATPLWII²⁰⁵GWGFTKQNGGKMSDILLQASVQV 350
 MTSP4-S 516 VALLQLDHPV[▽]VSAAVRPVCLPARSHFFEPGLHCWITGWGALRE-GCPTSNALQKVDVQV 574
 MTSP4-L 660 VALLQLDHPV[▽]VSAAVRPVCLPARSHFFEPGLHCWITGWGALRE-GCPTSNALQKVDVQV 718
 MTSP6 305 IALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATED-GCDAS[▽]PVLNHA²⁰⁵AVPL 363

 MTSP3 351 IDSTRCNAD[▽]DAYQGEVTEKMM²⁰⁵CAGIPEGGVDTCCQD²⁰⁵SGGPLYQSDQ--WHVVGIVSWGY 408
 MTSP4-S 575 IPQDLCS--EVYRYQVTPRMLCAGYRKGKKDACQD²⁰⁵SGGPLYCKALSGRWFLAGLVSWGL 632
 MTSP4-L 719 IPQDLCS--EVYRYQVTPRMLCAGYRKGKKDACQD²⁰⁵SGGPLYCKALSGRWFLAGLVSWGL 776
 MTSP6 364 ISNKICNHRDVYGGII[▽]SPSMLCAGYLTGGVDS²⁰⁵CQD²⁰⁵SGGPLYCQERR-LWKLVGATSFGI 422

 MTSP3 409 GCGGPSTFGVYTKVSAYLNWIYNVWKAEL 437
 MTSP4-S 533 GCGRPNYFGVYTRITGVISWIQQVVT 658
 MTSP4-L 777 GCGRPNYFGVYTRITGVISWIQQVVT 802
 MTSP6 423 GCAEVNKPFGVYTRVTSFLDWIHEQMERDLKT 453

[▽] cleavage site

+ potential glycosylation site

* unpaired cysteine

FIGURE 4